General version 5.1.3 Copyright (c) 1993 - 2003 Copyright Ltd

OM protein : protein seatch, using sw model

January 16, 2003 (1942:17), Smarch time 9 21429 Seconds Pun on:

(without alignments) 58.517 Million cell updates/sec

US-09-856-070-25

1 MI.RI,Q 5 Title: Perfect score: Sednence: Scoring table:

BLOSUM62 Gapop 10 0 , Gapext 0.5

283224 scqs, 96131422 residues

Total number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Ma+ch N9 Maximum Match 100%

Database :

pirl:* pir2;* pir3:*

Pred No. 1s the number of results predicted by chance to large a score greater than of equal to the source of the result being printed, and is derived by analysis of the total score distribution.

STIMMAPIES

		Description	hypothetical profe		conserved hypothet,	ribosomal protein	_	ribosoma) protein	ABC transporter, A	ABC transporter, A	gene 8 protein - e	gene 8 protein	B. subtilis YibH p		lin depen	aspartute carbamo;	aspartute carbamoy	aspartate carbamoy	U2 STRNP 40K prote	DNA Polymerase [1]	aspartate carbance	aspartate carbamoy	aspartate carbame,	probable from ARC	(AY007523) asbarta	hypothetical 43.6K	- 1	hypothetical prote	hypothetical prote	mitochondrial proc	_
		1.0	F72450	1169461	A71300	R5HT19	A36554	A48992	AF1561	AG1204	836703	WEBEA7	AB1553	AINTIGE	T41101	AP2737	1182583	AE3593	536335	1383655	P87552	A56144	1183595	F96620	B97518	095958	p91241	586132	BE4419	142428	S61455
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		η. 1 Α.1	୍ୟ	145889	enivod . nira
		586	-4	A34400	ezrin (validated)
35. 23		586		B41129	czrin - mouse
		019	C4	T19333	hypothetical prote
		0.53	r 4	147177	hypothetical prote
		748	~	T49633	glucan 1,4-alpha-d
77		785	CI	38038	Erpothetical prote
23		G ∩ 5	C4	T00475	probable disease
11 23		1428	C1	T39475	probable AIP depen
		1690	C1	T13030	microtubule bindin
3 21		100	C	A81097	primosoma! replica
1 21		100	7	C81845	primosomal replica
5 21		109	~	H95038	hypothetical prote

RESULT 1 F72450

hypothetical protein ArB2250 Aeropyrum pernix (strain KI)

Cispecies: Aeropyrum pernix Cipato 20-Ang 1999 #sequene_rowision 20-Ang-1999 #text_chang. 69 Jun 2030 C; Accession: F72450

E;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999
A. Litie. Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A, Reference number, A72450; Mulb:199310319; PMID:10382956
A;Accession: F72450

A;Status: preliminary

A; Molecule type: DNA

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A.Experimental Source: Strain K1 C.Gentlics: A.Gene: APE2250 C.Superfamily: Aeropyrum pernix hypothetical protein APE2250

0; Gaps Query Match 199-9%; Score 23; DH 2; Longth 120; Hest Local Similarity 100-0%; Pred. No. 35; Matches 5; Conservative 0; Mismatches 6; Lodels 6, Indels 0, Mismatches

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1 MLRLQ 5

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H69461

¿diserved hypothetical protein AF1697 - Archaeoglobus fulgidus C.Species. Archaeoglobus fulgidus C.Satz. 65:New 7397 #sequent-Invision of important attact_change of act-1999 C.Aa. ession: M69461

E.K. Fern, M. C. C. C. C. C. C. Lonb, J.F., White, O., Neison, K.E., Ketchum, K.A., Dod J. Fleischmann, K.E., Quackenbash, J., Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E. Glodek, A. Shou, t., Gverherk, R.; Bergyer, J.F., Werdman, J.F.; McDonald, L. Nature 390, 364–370, 1997.

A.Authors. Otterback, L.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.G., Werser, C.K., Venter, J.C.

A.Authors. Grouplete genome sequence of the hyperthermophilic, sulfate-reducing arch A. Peference complete.

A.Status, preliminary, ruchely acid sequence not shown, translation not shown

A,Mojecuie type: DNA A,Keuidaes, 1 157 - KLEZ A Cross-references: GR-AFDOORME, GR:AEDOU/NZ; NID:qzndszub; PIDN:AAB89957.1; PID:qz64 C.Saperiamily, Methanococcus januaschal conserved nypolaelical profein MJ1553

100 08, Scott 23; UB 2, wength 157; Sugry Match 0

Caps

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A;Title: Nucleotide sequence of mouse L19 ribosomal protein cDNA isolated in screenin A;Peterence number: A35554; MUID:91090840; PMID:1/02292
A;Accession: A36554
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Cancar Res. 53, 1408 1408, 1993
Astitle: High-level expression of the ribosomal profess in human breast tumors the
A;Reference number: A48992; MUID:93185086; PMID:8095182
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A.Experimental source: breast cancer cell line, MCF-75671; NCB:P:127872
A:Note: sequence extracted from NCB! backbone (NCB:N:127871; NCB:P:127872)
R:Kumabe, T.; Sohma, Y.; Yamamono, T.
Nucleic Acids Res. 20, 2598, 1992
A.Tille: Human cDNAs encoding elongation factor lgamma and the ribosomal protein LP9.
A:Reference number: S22655; MOID:92282147; FMID:1598220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tibosomal protein L19 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change l3-Aug-1999
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C:Date: 19-Dec-1993 *sequence_revision 18-Nov-1994 *text_change 13-Aug-1999
C:Accession: A48992; S22656
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A;Note: this sequence was submitted to the EMBL Data Library, December 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A/Cross-references: GB:MF2952; NID:a198642; PIDN:AAB48630.1, PID:a198643
C;Superfamily: rat ribosomal protein E19
C;Keywords: protein blosynthesis, ribosome
                                                                    A)Cross-references: GB:M30264; NID:q205112; PIDN:AAA41503.1; PID:q554467
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DNA Cell Biol. 9, 697-703, 1990
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                                                                                                                                                                                                                                                                                                                    100.0%; Score 23; DB 1; Length 196; 100.0%, Pred. No. 58;
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Matches 5; Conservative 0; Mismatches
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C:Superfamily: rat ribosomal protein 1.19
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A;Residues: 1-196 <HEN>
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   A;Molecule type: DNA
A,Rusidues, 117 145 KR12*
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A;Residues: 1-196 <NAK>
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C.hate: 30 Jun-1991 Ascaptence revision 30-Jun-1991 #text_change 21-Jui-2000
C.hate: 30 Jun-1991 Ascaptence revision 30-Jun-1991 #text_change 21-Jui-2000
C.Acressiou: A25710: A44989; A56646; I59124; S09560
Richan, Y.L.; Lin, A.; McNally, J.; Peleq, D.; Meyuhas, O.; Wool, I.G.
J. Biol, Chem. 252, Juli-1115, 1987
A.Hille: The primary structure of rat ribosomal protein L19. A determination from the science number: A26710; MULD:B7104220; PMLD: 3542997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riffaser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, E.; Gwin
Tson, J.; Khaladak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; NeDo
They, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 475-486, 1998
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A:Cross references: GB.AEG01239- GB.AEG00520; WED-33222937; PIDM-AACE5623 1; PID-3332294
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A;Reference number: A56846; MILD:45309903; DMLD:7789970
A:Aceession: A56845
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Proc. Natl. Acad. Sci. U.S.A. 86, 6691-6695, 1989
A.Tiller A Strategy to detect and isolate an intron-containing gene in the presence of A.Retorence number: 1991%4; MUID:87314; PMID:2771953
A.Retorence number: 1991%4; MUID:89367314; PMID:2771953
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A:Note: the differences in the central region are due to a fram.shift crio: resulting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Title: Complete genome šeguence of Freponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MJD:98332770; PMID:9665876
A:Accession: A71300
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Cisperius: Troponema pallidum subsp. pallidum (syphilis spirochete)
Cibate: 24 · ul 1908 #sevpuener_registes 24 · U] (1998 #fext_change 28 Jsi-2000
CiAccession: A71300
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                                    Caps
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A;Mesidues: 4-12 «CHA2»
A;Note: the protein is designated as ribosomal protein L19
R;Davies, B.; Protein, Molecular designated as ribosomal protein L19
Genomics 25, 3-2, 80, 1995
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Bost Local Similarity 100.0%;
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                                                                                                                                                                      94 MI.RI.Q 98
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                                                                                                     1 MURLO 5
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A.Status, preliminary, translated from ObjemblyDUBHJ
"NaMulecule type: DNA
"N.Molecule t
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C:Species: equine herpesvirus 4
C.Date - 89-Tuni1994 #sequencinoistes is May 1995 #text_change Lital 2000
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C/Accession: 136795
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A.cross-references: EMBL:X17684; NID:g312459; PIBRICAA35668.1; PID:g59216
A:Cross-references: EMBL:X17684; NID:g312459; PIBRICAA35668.1; PID:g59216
E:Tellond, E.A.; Malson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.
J. Gen. Virol. 79, 1197-1205, 1998
A:Tille: The DNA sequence of equine herpesvirus-4.
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A,Kresidues: 1.245 <TEL>
A,Cress-reterences: GBLM86664: NID:q330791; PIDN:AAB02443.1; PID:q330800
A,Cress-reterences: GBLM86664: NID:q330791; PIDN:AAB02443.1; PID:q330800
R(Tellord, E A P : Watson, M S : McBride, R : Davison, A.J.
Virology 189, 304-316, 1992
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Arritle: The DNA sequence of equine herpesvirus-1.
A.Reference number: A41831, MOID:92295566; PMID:1318606.
A.Gontenis: annotation: possible protein-roding trames.
A.Rote: neither amino acid nor nucleotide sequence is given.
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submitted to GenBank, March 1992
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A;Accession: 136795
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A, Accession. 142551
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C;Superfamily: varicella zoster virus genc 7 protein
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A:Note: host Equus caballus (domestic horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                   gene 8 protein - equine herpesvirus 4
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nes 5; Conservative
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A;Accession: 536703
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Actions: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; MaitGurnam, A., Ma ok, T.; Schlucher, Y.; Simmes, M.; Tetres, A.; Vadqued-Baland, J.A.; Vuss, H.; Wehland, A.Title: Comparative genomics of Listeria species.
A.Title: Comparative genomics of Listeria species.
A.Accession: AF161
A.A
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Science 294, 849-852, 2001

Anthors Kreft, J. Kohn, M., Konst, F., Kurapkat, G.: Madueno, E.: Maltourdam, A.: Ma Anthors Kreft, J. Kohn, M., Torrez, A.: Vagquez-Boland, J.A.: Vass, H., Wehland, A.: Reforence number: AH1077; Mutn. 215,7274; pwin. 11679669

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Astrockasion and Astrockasion and
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R;Glaser, B., Prandenl, L., Buchrieser, C., Amend, A., Boquers, E., Berche, P., Bluecker
J. Dominguez-Bernal, G.; Duchaud, E.; Duraud, L.; Dussurget, O.; Entian, K.D.; Flain, H.
D.; Jones, L.M.; Karst, U.
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C.Species: Listeria monocytogenes
C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
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C.Date: 27:Nor 200] #segacha__refstan 27:Nov 200 #faxt__darge 27 Nov 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
A;Cross-references: GDH:128847; OMIM:180466
                                                                                                                                                                                 C:Keywords: protein biosynthesis: ribosome
                                                         A:Map position: 17q11-17q11
C:Supertamily: rat ribosomal protein L19
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Matches 5; Conservative C
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5; Conserva
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aspartate carbamoy) transferase (imported) Agrobacterium tunnefaciens (strain 058, D. C.Species. Agrobacterium tunnefaciens
C.Species. Agrobacterium tunnefaciens
C.Date: 11-Tan-2002 *Sequence_revision 11-Jan-2002 *text_change 01 Peb-2002
C.Accession: AD2237
R.Wood, D.W.: Setubal, J.C.: Kaul, R.: Monks, D.: Chen, L.: Wood, G.E.: Chen, Y.: Wooderage, G.: Gillet, W.: Grant, C.: Guenthner, D.: Kutyavin, T.: Levy, R.: Li, M.: McCl. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A)Gene: pyrB
A:Map position: circular chromosome
C.Superfamily, ornithine carbamoyltransferase, aspartato/ornithine carbamoyltransfera
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R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq A;Title: The qenome sequence of the plant pathogen Xylella fastidiosa.
A;Title: The qenome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: AR515: Millo:20367717; PMID:1091047
A,Nette: for a complete list of authors see reference number A59128 below
A,Nettesion. H82583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumelaciens C58.
A:Reference number: AB2577, FWHD:11743193
                                                                                                                                                                                                                                       A;Residues: 1-288 «PUR»
A:Cross references: DMBL:AL031535, PIDA.CAA20758.11, GSPUH:GN00068; SPUH:SPCT1664.11
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C:Species: Xylella fastidiosa
C:Date: 18-Ang-2000 *sequenc_revision 20-Aug-2000 *text_change 02 Sep 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Superfamily: kinase-related transforming protein; protein kinase homology
C;Accession: T41101
R;Purnelle, B.; Gotteau, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMHL Data Library, September 1998
A;Reforence number. 221964
A;Accession: 141101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 23; UB 2; Length 288;
100.0%; Pred. No. 87;
                                                                                                                                                                       A/Status. Freliminary, translated from GB/EMBL/DDBJ
A/Molecule type: DNA
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A,Molecule type: DNA
A,Fesidaes: 1-313 aKUR
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|222 MI.RIQ 226
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A:Gene: SPDI
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Actuthors: Kreft, J.; Kuim, M.; Aumst, A.; Aurapkat, G.; Madueme, F., Maiteurnam, A.; Ma ok, C.; Schluster, T.; Simose, N.; Terrez, A.; Vazquez Boland, J.A.; Voss, H.; Wehland, A.; Malitle: Comparative genomics of Listeria species.
A:Reterence number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                         Riddascr. D. Françoul, L.; Buchricser, G.; Amend, A.; Baguero, F.; Berehe, P.; Hioceker C.; Dominquez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.; Science 294, 849 822, 2021.

Asauthors: Kreff, J.; Know, M.; Knust, F.; Kurapkat, G.; Maduemo, F.; Maitentram, A.; Machors, R.; Herrez, A.; Vargaer-Beland, J.A.; Voss, H.; Wehland, A.H.; Comparative genomies of listeria species.

Astelletence number: ARIO77-MHTD-21547279; PMID-11673669
                                                                                                                                                                                                     b. subtilis Yjbli protein homolog lin0963 [imported] - Listeria innocua (strain Clip11262 Cyspecies: Listeria innocua (clidate: 27 Nov-2001 #sequence_revision 27 Nov-2001 #text_change 27 Nov-2001 Cydrevssion: AH1553
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.; Dominquez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, B.
D.; Jones, L.M.; Karst, U.
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A;Experimental source: strain EGD-e
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A:Experimental source: strain Clip11262
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C:Date: 27 Nov 2001 #scquence_revision 27 Nov 2001 #text_change 27 Nov 2001
C:Aeression: ADI195
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Cibate: 03 Dec:1999 #sequence_revision 03-pac-1999 #text_change 31-1an-2000
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100.0%; Pred. No. 82;
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Matches 5: Conserv
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A: Rossidues: 1-322 <SIM>
A: Cross references: GB: AE004055; GB: AE003849; NID: g9107371; PIDN: AAP85025.1; GSPDH: GN001
A: Experimental Source: strain 955
R: Simpson, A.J. G.: Reinach, E.G.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R. S.; Bueno, M.F. F.; Filloner, E.A.; Garraro, D.M.; Carrer, B. Briones, M.R. S.; Bueno, M.F.; Filloner, E.A.; Gerrer, B. Briones, M.R. S.; Bueno, M.F.; Ferrer, J. A.; Franca, S.C.; Franca, G.C.; Frohm A. Authors: Perreira, June 2000
A. Authors: Perreira, V.C.A.; Ferre, J. A.; Fraya, J.S.; Franca, S.C.; Franca, M.C.; Frohm J.D.; Junequeira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laid Grado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F. M.F.; Oliveira, M.A.; de Oliveira, M.C.; Jed. Oliveira, M.C.; Painnis, F. A.; Authors: Martins, F. M.F.; Oliveira, M.A.; de Oliveira, M.C.; Jed. Oliveira, M.C.; Jed. Oliveira, M.C.; Jed. Oliveira, M.C.; Jed. Oliveira, M.A.; Ad. G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; de Sar, K.G.; Santelli, R.V.; Sawasak A; Muthors: annotation
A. Kelerence number: A59328
A. Contents: annotation
A. Gonefica: XY226
C. Superfamily: ornithine carbamoyitransferase; aspartate/ornithine carbamoyitransferase

Query Match
Best Local Similarity 100.0%; Score 23; DB 2; Locath 322;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 5; Conservative 0; Mismatches 0; Indels
Qy 1 MURLO 5

or Caps

Search completed: January 16, 2003, 16:57:53 Job time: 9.21429 secs ---

